

FIGURE 1

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGCCCCGCGCCCAG
TC**ATG**ACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGCTGCTCAGTGCGGCGGTGTGCCGGG
CTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCAT
GTGCCGAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTG
ACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGTC
TTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGGAAAACGGGGATTTC
CACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGC
TAAAGCTGGTGAAGGGCATTTCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATC
ACCTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAA
AGAAA**TAA**TAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGCCCCGCGCCCAG

CGCGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCAGGGAGTGTCCCGGCTGGCCCTAGG
CAGGCAGCCGCACCA**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCTGCTCAGCTTCTTGGGCATGGTGGGCA
CGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTT
ACCTGAAAGGGCTCTGGATGGAGTGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGC
TGGCGCTGCCCCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCG
CTTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTGCCATCCTCG
GCGGCACCCTCTTCATCCTGGCCGGCCCTCCTGTGCATGGTGGCCGTCTCCTGGACCACCAACGACGTGGTGCAGA
ACTTCTACAACCCGCTGCTGCCCAGCGGCATGAAGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCT
CGTCCCTCTCGCTCATTGGTGGCACCCCTGCTTTGCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGG
CCCCGCCCAGGGCCACCACGACCACTGCAAAACCCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATC
GGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG**TGA**GTCCTCCACAGCCTGCT
TCTCCCTTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGGTTCCAGCACAAAGTTTAC
TTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGG
AAATAAGAGGAGGAGAAAGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATAT
ATATTTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGAAGTGGGAGTTTGGTCAGTGGGGTTGGTTTGTG
ATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 3

CAGGACCAGGTCTTCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
 ATCCTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG
 GAGAAGCCACTGCCCCACCGCTTCTTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCTGACTGGCTGAAGCTG
 CGCATGATCCGTTCTGAGGTGCTCCGCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG
 TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCTGGACCAGGCAGTGGCCCCAC
 GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC
 GGCGCTCCGGAGGCCAGACTTTCACCTCCTTGCTCACAGCCTCCCTGCCGCCCCGCCGAGACAGCACAGAGGCA
 CCCAAACCAAAGAGCAGCCAGAGCAGCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTG
 GGCCCTGAGGACGACCTGGCTGGCATGTTCTCCAGATTTTCCGCTCAGCCCCGACCCTCGGTGGCAGAGCTCC
 AGTCCCCGCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCCGCTCGTCCAGGGCAGCCCC
 GAGGTGCCGGGCATCACGGTGCGTGTCTGCAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGCGGTGCCCTG
 GTGATGTCCATGCACCGTAGCCACTTCTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG
 CCACAGGACACCGGCTTCTCCTCGCTCTTCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC
 GTGGAGGGCGGGCCCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCCTCAGCCGGGCGCAGGCTCAGTGAT
 GTGCGAGGGGGGCTCCTGCGCCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTTCAGCTCCACCGTC
 CGTGCCGTCATCGCCACCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGACCTGATCAGCAAAGTCTCCAG
 GGGCTGATCGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC
 TCCCCGTTTCCAGCCTGTAAGCCCGTTGTGGTGGTGAAGTCCCTGCTGCTGCAGGAGGAGGAGCCCCCTGGCTGGG
 GGGAAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCTCGTCAGGCCCTCCTAGTGGACTGG
 CTGGAAATGCTGGACCCCGAGGTGGTCAGCAGCTGCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGAGGAAG
 GGCAAAGGTGAGGCCAGGTGCCCTCGTTCCGTCCCTACCTCCTGACCCTCTTACGCATCAGTCCAGCTGGCCC
 AACTGACACAGTGCATCCGAGTCTGCTGGGCAAGAGCCGGGAACAGAGGTTTCAGCCCTCTGCCTCTCTGGAC
 TTCTCTGGGCCTGCATCCATGTTCTCGCATCTGGCAGGGGCGGGACAGCGCACCCCGCAGAAGCGGCGGGAG
 GAGCTGGTGTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG
 AGCCAGGACGGGGACACAGCCGCCCTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG
 GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGGA
 AGGCGCTGCCGAGACCTTCTCCTGCAGCTCTACCTACAGCGGCCCGGAGCTGCGGGTGGCCGTGCTGAGGTCTTA
 CTGCACAGCGAAGGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCACGCTCCTT
 GCGGACACCAGCGACTCCCCGGGCGTTGGAGAACCAGGGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG
 GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCCTGCACGGCCGCACCCACCTCAACTTC
 CAGGAGTTCCGGCAGCAGAACCACCTGAGCTGCTTCTGCACGTGCTGGGCCTGCTGGAGTGTGCTGCAGCCGCAC
 GTGTTCCGCAGCGAGCACACAGGGGGCGCTGTGGGACTGCCTTCTGTCTTCATCCGCCTGCTGCTGAATTACAGG
 AAGTCTTCCCGCCATCTGGCTGCCTTCATCAACAAGTTTGTGCAGTTCATCCATAAGTACATTACCTACAATGCC
 CCAGCAGCCATCTCCTTCTGCAAGACGCGGACCCGCTCCACGACCTGTCTTCGACAACAGTGACCTGGTG
 ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGCCAGCAGGGACGACAGGACCGACCGAGGCCTGGACGAAGAG
 GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGGCCCTGGTCAAGCTCTCCTGTTACCCCTCTGACCGCGGCCGAG
 ATGGCCCCCTACATGAAACGGCTTTCGCGGGGCAACCGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
 GAGATGTCCCGGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
 GAGTGTGCGCAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTC
 CTGCCCACGTTTCATGTAAGTCTGGGCGAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG
 TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCTTCTGGTGGGCATGTACGGCCAGATG
 GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGCCTGTGGCAGCCGA
 CCCCCCTCCAAGCCCCGGCCCTCCCGTCCCCGGGGATCCTCGAGGCAAGCCAGGAAGCGTGGGCGTTGCTGG
 TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGCAGGCCAGGAGCAATACTCCGAGCCCTGGGGTGG
 CTCCGGGCGGCGGCTGGCATCAGGGGCCGTCCAGCAAGCCCTCATTACCTTCTGGGCCACAGCCCTGCCGCGG
 AGCGGCGGATCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAAGTGTCAA

FIGURE 5

MTLRPSLLPLHLLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHIHYTGSLVDGRIID
TSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGFPSPVPADAVVQYDVELIALIRANYWL
KLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVSKKKLKEEKRNSKKK

Signal peptide.

amino acids 1-25

Transmembrane domain.

amino acids 155-174

N-glycosylation site.

amino acids 196-200

N-myristoylation site.

amino acids 95-101

Amidation site.

amino acids 119-123

FKBP-type peptidyl-prolyl cis-trans isomerase signature 1.

amino acids 62-78, 87-124, 128-142

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FIGURE 6

MASTAVQLLGFLLSFLGMVGTLLITTLPHWRRTAHVGTNILTAVSYLKLWMECVWHSTGIYQCQIYRSLALPQ
DLQAARALMVISCLLSGIACACAVIGMKCTRCAGKTPAKTTFAILGGTLFILAGLLCMVAVSWTTNDVVQNFYNP
LLPSGMKFEIGQALYLGFISSSLIGGTLCLLCLSCQDEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSV
TSATHSGYRLNDYV

Signal sequence.

amino acids 1-21

Transmembrane domains.

amino acids 78-98, 116-136, 162-182

N-myristoylation sites.

amino acids 17-22, 20-25, 60-65, 92-97, 101-106, 178-183

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 85-95, 87-97

PMP-22/EMP/MP20/Claudin family.

amino acids 4-181

FIGURE 7

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRMIRSEVLRLVDAAL
 QDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNYMAHLVEVQHERGASGGQTFHSLLTAS
 LPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLGPEDDLQAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQ
 ELARVVQGSPEVPGITVRVLQALATLLSSPHGGALVMSMRSHFLACPLLRLCQYQRCVPQDTGFSSFLKVL
 QMLQWLDSPGVEGGPLRAQLRMLASQASAGRRLSDVRGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQCSV
 EPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASFPACKPVVVSSLLLQEEEP
 LAGGKPGADGGSLEAVRL
 GPSSGLLDVLDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFRPYLLTLFTHQSSWPTLHQCIRVLLGKSRE
 QRFDPASLDFLWACIHVPRIWQGRDQRTQPQRREELVLRVQGP
 ELISLVELILAEAE
 TRSQDGD
 TAACSLIQAR
 LPLLLSCCCGDD
 DESVRKVTEHL
 SGCIQQWGD
 SVLGRRCRDL
 LLQLYLQ
 RPELRVPV
 PEVLLHSEGA
 ASSSVCKLD
 GLIHRFITLLADTSDSRALENRGADASM
 ACKLAVAHPL
 LLLRHLPMIA
 ALLHGRTHLN
 FQEF
 RQQNHLSCFLHV
 LGLELLQPHVFRSEHQ
 GALWDCLLS
 FIRLLLNYR
 KSSRHLAA
 FINKFVQFI
 HKYITYNAP
 AAISFLQKH
 ADPLH
 DLSFDNSDLV
 MLKSLLAGL
 SLPSRDDRT
 DRGLDEEG
 EEEESSAG
 SLPLVSVS
 LFTPLTAA
 EMAPYMKR
 LSRGQTVE
 DLLEVLSDI
 DEMSRRR
 PEILSFF
 STNLQRL
 MSSAECC
 RNLAFSL
 ALRSMQ
 NSPSIAA
 AFLPTFM
 YCLGSQ
 DFEV
 VQTALRN
 LPEYALL
 CQEHA
 AVL
 LHRAFL
 VGM
 YQMDPS
 AQISE
 ALRIL
 HMEAVM

Signal peptide.

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449, 665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 8

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF
SMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSC
MIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

Signal peptide.

amino acids 1-28

Transmembrane domain.

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220, 220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

Immunoglobulin domain.

amino acids 49-132

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